REMARKS

Support for claims 35 and 36 can be found throughout the specification, e.g., Page 11, lines 22-29; Page 22, lines 5-7; Page 28, lines 35-37; Page 30, lines 30-35.

8. It is requested that this drawing requirement be held in abeyance until subject matter is deemed allowable.

9. The hyperlinks have been deleted.

10. Applicant will correct the trademarks in due course as requested.

11. The ATCC address listed on Pages 26 and 32 of the specification has been corrected.

12. Claims 19 and 20 have been corrected.

13-14. Since no patent has issued on either application, a terminal disclaimer is not appropriate at this time.

15-16. **Rejection under §112, first paragraph**

Applicants have identified BVH-P7 DNAs and proteins from S. pyogenes. They have demonstrated that these proteins have a number of properties that make them useful. For example, it was shown that a BVH-P7 protein protects mammals against S. pyogenes infection. See, e.g., Examples 7 and 8 on Pages 31-35 of the specification.

The specification describes the identification of ten different homologues of the BVH-P7 gene. See, e.g., Specification, Page 3, lines 14-20; Page 27, Table 2. These homologues show a high degree of sequence identity. For example, Fig. 3 compares the amino acid sequences from

seven different strains of S. pyogenes. As indicated, they are highly conserved, sharing 95% or more sequence identity along their sequenced lengths. See, attached Exhibit A.

According to *University of California v. Eli Lilly*, 43 USPQ2d 1398, 1407 (Fed. Cir. 1997) and the PTO's own Written Description Guidelines, "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNA, defined by nucleotide sequence, falling within the scope of the genus or of recitation of structural features common to the member of the genus." *Synopsis of Application of Written Description Guidelines*, Page 31. This would be similarly true for polypeptides. (Compare Example 8 on Page 33 of the *Guidelines*.) Thus, the question is whether an Applicant has provided a sufficient number of sequences to establish that they have possession of a genus of proteins that share structural features and/or conserved sequence identity. See, e.g., Guidelines, Page 33, line 14; Page 36, lines 19-21. In other words, do the sequences "represent" a genus which they are entitled to claim?

This is clearly the case here. Applicants have disclosed a number of amino acid sequences that code for the S. pyogenes BVH-P7 protein. Fig. 3 provides clear evidence that significant sequence identity is shared between them, and that they are structurally related and show little sequence variation. Thus, it is evident that Applicants have identified a sufficient number of representative BVH-P7 polypeptides to support the claims.

Furthermore, Example 9 on Page 35 of the *Synopsis of Application of Written Description Guidelines* provides an example of a genus claim which is supported by isolation of "nucleic acids" by hybridization which were not sequenced, but were shown to have the activity of the single disclosed cDNA. The BVH-P7 sequences described in the present application were also isolated by hybridization (used in combination with PCR, as described on Page 26, line 16-Page 25 of the Specification). These, and other BVH-P7 sequences, were shown to be highly conserved (Fig. 3) and therefore would have the antibody/immunological activity described for SEQ ID NO: 2. The information disclosed in the present application therefore satisfies the

requirements set forth in the Patent Office's own materials.

The discussion on Pages 6-8 of the Office action alleging that it would require undue experimentation to determine "the effect of different substitutions and the nature and extent of the changes that can be made" is not determinative. First, the PTO's own guidelines say that as long as a representative number of species are disclosed, claims are enabled for their full scope. See, above. This is consistent with the *Eli Lilly* case cited above.

Moreover, the examiner's focus is misplaced. The presence of inoperative embodiments within the scope of a claim does not necessarily render a claim non-enabled. The standard is whether a skilled person could determine which embodiments that were conceived, but not yet made, would be inoperative or operative with expenditure of no more effort than is normally required in the art. Atlas Powder Co. v. E.I. du Pont de Nemours & Co., 750 F.2d 1569, 1577, 224 USPQ 409, 414 (Fed. Cir. 1984); MPEP 2164.08(b). The specification provides clear guidance on how to isolate polypeptides that fall within the scope of the claims, and uses this information to successfully identify many different sequences, e.g., illustrated in Fig. 3.

17-18. The term "analog" has been canceled from the claim since it is redundant to the recited sequence identity. Therefore, the scope of the claim has not been changed by this amendment.

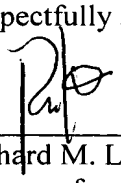
The claim has been amended to clarify that the claimed polypeptide is selected from the recited list.

19-20. Bjorck et al. (WO99/52939) does not disclose a polypeptide having the claimed characteristics, e.g., fragments comprising at least ten contiguous amino acids.

In view of the above remarks, favorable reconsideration is courteously requested. If there are any remaining issues which could be expedited by a telephone conference, the Examiner is courteously invited to telephone counsel at the number indicated below.

The Commissioner is hereby authorized to charge any fees associated with this response or credit any overpayment to Deposit Account No. 13-3402.

Respectfully submitted,



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Attorney Docket No.: PHARMA-0018

Date: August 25, 2004

EXHIBIT

A

Table A. BVH-P7 homology between different GAS strains

	Spy74_M3	Spy70_M5	Spy69_M6	Spy68_M2	Spy60_M1	12357_M18	700294_M1	12384_M3	Spy67_M6	B514 (s. murine)
Spy74_M3	XXXX									
Spy70_M5	97.4 (99.4)	XXXX								
Spy69_M6	98.1 (99.4)	99.1 (99.8)	XXXX							
Spy68_M2	97.0 (99.1)	99.0 (99.1)	98.2 (99.1)	XXXX						
Spy60_M1	97.2 (99.3)	99.4 (99.5)	98.7 (99.5)	99.4 (99.4)	XXXX					
12357_M18	97.6 (99.5)	99.8 (99.9)	99.3 (99.9)	99.0 (99.2)	99.4 (99.6)	XXXX				
700294_M1	93.7 (99.3)	95.5 (99.5)	95.0 (99.5)	95.7 (99.4)	96.3 (100.0)	95.7 (99.6)	XXXX			
12384_M3	98.3 (100.0)	98.9 (99.4)	99.0 (99.4)	98.5 (99.1)	98.7 (99.3)	99.1 (99.5)	95.0 (99.3)	XXXX		
Spy67_M6	97.6 (99.3)	99.2 (99.7)	99.5 (99.9)	98.4 (99.0)	98.8 (99.4)	99.4 (99.8)	95.1 (99.4)	99.3 (99.3)	XXXX	
B514 (s. murine)	97.1 (99.1)	99.0 (99.2)	98.4 (99.1)	99.1 (99.2)	99.3 (99.4)	99.1 (99.2)	95.6 (99.4)	98.6 (99.1)	98.5 (99.0)	XXXX

Some of the sequences in the application are disclosed with the leader sequence, some not.
The first value represents the homology between 2 sequences that can be of different length.
The second value in parentheses represents the homolgy between 2 sequences having the same length.